Viability Status of Oregon Salmon and Steelhead Populations in the Willamette and Lower Columbia Basins

Part 1: Introduction and Methods

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Introduction

This report describes the current status of salmon and steelhead in Oregon Lower Columbia River tributaries, including the Willamette River. This region contains six groups of salmon and steelhead listed as threatened under the US Endangered Species Act (ESA): Lower Columbia River (LCR) chinook, Columbia River (CR) chum, LCR coho, LCR steelhead, Upper Willamette (UW) chinook, and UW steelhead. For salmon, the listed group is referred to as an Evolutionarily Significant Unit (ESU) and for steelhead, the listed group is a Distinct Population Segment (DPS) (Waples 1991, NMFS 2006). The LCR chinook ESU, CR chum ESU, LCR coho ESU and LCR steelhead DPS include populations that spawn in tributaries on both the Oregon and Washington sides of the Columbia River. This report, however, deals only with the populations spawning in Oregon tributaries. The status of Washington populations is discussed in the Washington Lower Columbia recovery plan (Lower Columbia Fish Recovery Board 2004) and elsewhere (McElhany et al. 2004). The UW chinook ESU and UW steelhead DPS are wholly contained in the Willamette River Basin of Oregon and all their component populations are addressed here.

The primary reason for conducting this assessment is to inform salmon recovery planning in Oregon. Information on individual population status is useful in scoping the level of effort needed to improve population status and reach recovery goals. It can also be useful in prioritizing populations and actions for recovery efforts. Another purpose of this report is to evaluate proposed viability criteria. Viability criteria describe what to measure to evaluate extinction risk ('metrics') and levels of the metrics associated with a low extinction risk ('thresholds'). These viability criteria are meant to inform delisting criteria for ESA listed species (NMFS 2000). In April 2006, the Willamette/Lower Columbia Technical Recovery Team (WLC-TRT) distributed revised draft viability criteria (McElhany et al. 2006a)[1]. By applying the viability report thresholds in this current status evaluation, we explored the utility of the 2006 draft criteria.

It is useful to consider the distinction between setting recovery goals and conducting a current status assessment. The viability criteria developed by the WLC-TRT are intended to inform recovery goals. Recovery goals are targets for the future and the goals tend to include either a very limited suite of metrics or are limited to describing guiding principles rather than quantitative thresholds. A current status evaluation, on the other hand, is concerned with providing an accurate view of where a population is at a given time and should utilize *all* available information. Existing data sets may contain information not identified as part of the viability goal metrics, but this information may still provide indicators of population status and should not be ignored. Accordingly, in this report we analyze both the viability criteria metrics and any other relevant data available.

Since the focus of the ESA is on extinction risk, in this assessment, we are equating the term "status" with "extinction risk." Although there may be alternative definitions of status (e.g., "harvestable"), this analysis is an evaluation only of population extinction

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[1] The April 2006 WLC-TRT revised viability report [ref] built on a 2003 WLC-TRT viability report [ref]. Unless otherwise noted, references in this document to the "viability report" refer to the 2006 version [ref].

risk. There is clearly a link between extinction risk and other definitions of status, but we do not explicitly consider such links.

Because we need to evaluate a diverse array of information types, the ultimate estimation of risk involves some level of professional judgment. Although our analysis was systematic and evidence-based, it was not based on a single quantitative algorithm. While using only a fixed set of quantitative criteria might have the advantage of clear repeatability, and a perception of objectivity, it is likely to be less accurate because it fails to take into consideration population specific information and information that is not readily quantified.

Population status (i.e., extinction risk) is a continuous variable from almost 0% chance (no risk) to 100% chance (certain extinction). Following the methods in the viability report, we partition this continuum into the general risk categories shown in Table 1. A population with a persistence probability greater than 95% over a 100-year period is termed "viable". This level of risk is consistent with VSP guidelines (McEhany et al., 2000), the conservation literature (e.g., NRC, 1995), and with informal policy guidance indicating that, at least initially, the appropriate recovery target at the population level would be no more than a 5 percent risk of extinction within 100 years. Although the categories are defined in terms of quantitative extinction risk, we can rarely estimate extinction risk with precision and the categories are qualitative indicators. Estimating extinction risk is a challenging exercise – we are attempting to predict events far into the future. It is essential when presenting information on population status to include some assessment of the uncertainty associated with the prediction. We include both quantitative and qualitative assessments of the uncertainty in our extinction risk estimates.

Table 1: Population persistence categories (copied from McElhany et al. 2006a).

Population Persistence Category	Probability of population persistence in 100 years	Probability of population extinction in 100 years	Description
0	0–40%	60-100%	Either extinct or very high risk of extinction.
1	40–75%	25-60%	Relatively high risk of extinction in 100 years.
2	75–95%	5-25%	Moderate risk of extinction in 100 years.
3	95–99%	1-5%	Low ("negligible") risk of extinction in 100 years (viable salmonid population).
4	>99%	<1%	Very low risk of extinction in 100 years.

In parts of this report, we include a description of results from the Oregon Native Fish Report (ODFW 2005). Although comparison of our analysis to the Native Fish Report is interesting, it is important to note the scope and limitations of the Native Fish Report. These are best summarized in the words of the Native Fish Report itself:

> "…This report summarizes risk assessment completed for native salmon and steelhead, most native trout, and other selected native fish species using the NFCP [Native Fish Management Policy] interim criteria. …. Risk, as used in this report, refers to the threat to the conservation of a unique group of populations in the near-term (5-10 years). …The NFCP interim criteria provide temporary guidance to ensure the conservation of native fish prior to completion of more detailed conservation plans for each species or group of populations. …The

interim criteria <u>do not</u> describe long-term, extinction risks such as continuing downward trends, increasing threats, or extended intervals of unfavorable environmental conditions. Such long-term risks are better assessed with more in-depth analyses than was conducted for this report and will be considered in conservations plans."

Our report is a more comprehensive analysis with a longer time horizon than the Native Fish Report.

This analysis has been conducted as a joint project of the NOAA Fisheries Northwest Fisheries Science Center (NWFSC), the Oregon Department of Wildlife (ODFW) and Cramer Fish Sciences (under contract to ODFW). Although the report has benefited from review and consultation with other biologists, both inside and outside our agencies, the final evaluations are those of the report authors, which may or may not reflect agency opinion.

Methods

Methods Overview

The majority of the methods used in the report are described in the WLC-TRT viability report (McElhany et al. 2006a), which builds on the basic framework in the NOAA Technical Memorandum on Viable Salmonid Populations (VSP (McElhany et al. 2000)) and a previous WLC-TRT interim viability report (McElhany et al. 2003). The methods described below are largely a summary of the viability report and readers are encouraged to examine the viability report for a more complete discussion. Since the viability criteria relate to evaluating risk status under the ESA, we are ultimately concerned with the status of the ESU/DPS (since the ESU/DPS is the listed unit, recovery criteria apply at the ESU/DPS scale). In the viability criteria, ESU/DPS status is assessed by examining the status of individual populations and groups of populations (called "strata") within a framework for ESU/DPS viability. Population boundaries for Pacific salmonids in the WLC have been identified in Myers et al. (Myers et al. 2006) and the population strata groupings are described in the viability report.

ESU/DPS Level Evaluation

Since this report is concerned only with the status of Oregon populations, it does not summarize status of the full Lower Columbia chinook and coho ESUs, steelhead DPS, or the Columbia River chum ESU, since those ESU/DPSs include some populations in Washington. The UW chinook ESU and steelhead DPS are both entirely in Oregon, so this report does analyze their status. The ESU/DPS criterion is that all historical strata need to be at a low risk of extinction. A low risk stratum is described as one with at least two viable populations (i.e. persistence category ≥3), where the average of the persistence categories for all historical populations is ≥2.25 based on the scale in Table 1, and there are sufficient viable populations to ensure that the stratum is buffered from the risks of catastrophic events, degraded metapopulation processes, and degraded evolutionary processes. Support for these recommendations is provided in the viability reports.

Individual population status is determined by examining three main attributes: 1) abundance and productivity (A&P); 2) spatial structure (SS); and 3) diversity (DV)[2]. These three primary attributes are sometimes referred to as the "biological" factors, or what we can learn from looking primarily at fish performance. A comprehensive evaluation of population status should also include an examination of the threats facing the population with an emphasis on future environmental conditions. Understanding future conditions is necessary to address the stationarity assumption inherent in the biological factor analysis. The stationarity assumption is that the recent past is a reasonable predictor of future fish performance. This assumption would be violated if future environmental conditions are different from the recent past (where "environment" is broadly defined to include anything that affects salmon). In this report, we do not conduct a complete assessment of likely future environmental conditions and their

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[2] The VSP report (McElhany et al. 2000) separates abundance and productivity into two separate attributes for a total of four attributes. Because the effects of abundance and productivity on extinction risk are so interconnected, we analyze them together.

predicted impacts on population biological status, which would involve examination of both current and potential population threats. In conducting the analysis, we largely rely on the stationarity assumption, but make some adjustments to evaluations of the three population attributes if a violation of the assumption seems likely (e.g., with regard to global climate change). A more thorough evaluation of likely future environmental conditions would greatly enhance population status evaluation.

ESU/DPS status was evaluated for each population on the 0-4 persistence category scale shown in Table 1. We estimated the overall population score by first evaluating on the same 0-4 scale each of the three primary population attributes (abundance and productivity, spatial structure and diversity). The 0-4 score for the individual attributes was based on what risk would be suggested by examining that attribute in isolation. The individual attributes are likely to be correlated, so these are not independent factors; however, each does contribute some unique information.

We relied on professional judgment to reach overall conclusions on risk status associated with each population's attributes based on consideration of any and all quantitative metrics available. Using a single, quantitative method for combining all of the available information did not seem a practical approach. To capture the uncertainty in our assessment, we present our conclusions as a probability distribution in the form of "diamond graphs" (Figure 1). These graphs are presented with the population risk categories on the vertical axis. The thickness of the diamond at any particular point indicates the relative probability of that risk category. The most likely risk category is shown by the thickest part of the diamond and the maximum and minimum likely risks are indicated by the upper and lower tips of the diamond. Although the risk probability diamonds are not generated by any quantitative algorithm, the presentation of the multiple quantitative analyses and any qualitative considerations leading up to the risk conclusions are intended to make the evaluation as transparent as possible.

Overall population scores were estimated from individual attribute scores by using a modification of the weighted average algorithm developed by the WLC-TRT. In the weighted average method, the 0-4 scores are averaged, with abundance and productivity weighted twice as much as the sum of the other two attributes because it is considered the better predictor of extinction risk (Equation 1).

Equation 1: popScore = 4/6*abud&ProdScore + 1/6*spaceScore + 1/6*diverScore

The weighted average approach integrates all three of the population attributes, but may give a misleading result in cases where the abundance and productivity is low even though spatial structure and diversity are not excessively degraded. In these cases, the population is likely experiencing some risk factor driving down abundance and productivity that is not reflected in the spatial structure and diversity score. In these cases, it is appropriate to evaluate the status of the population based on the low abundance and productivity, rather than incorporating all the attributes in a weighted average. We therefore applied the following rule:

> *If the abundance and productivity risk estimate is lower than the spatial structure or diversity estimate, use the abundance and productivity rating as the overall population rating, otherwise, use the weighted average method to set the overall population rating.*

With this rule, spatial structure and diversity ratings might make a summary score lower than the abundance and productivity score, but spatial structure and diversity ratings will not make the summary score higher than the abundance and productivity score. This method is more precautionary than always applying the weighted average algorithm.

We present the overall population status in the form of diamond graphs like those used to present individual attribute status. If the weighted average method is applied, a Monte Carlo approach is used to generate the diamonds. Independent values are randomly drawn from the diamond graph distributions of the individual attributes then averaged using Equation 2. This is repeated 10,000 times and the resulting distribution of population scores are presented as a diamond graph.

$$\text{Equation 2: popScore} = W_a * \text{abud\&ProdScore} + W_s * \text{spaceScore} + W_d * \text{diverScore}$$

In Equation 2, the parameters W_a, W_s and W_d replace the average weights of 4/6, 1/6 and 1/6 of Equation 1 because these weights themselves are estimated with uncertainty and are treated as random variables in the Monte Carlo process. The weights are constrained to sum to one and we used a random multinomial approach to describe the uncertainty in these parameters. This approach is described in Appendix A. We utilized a shape parameter of 50, which preserved the feature that abundance and productivity are generally weighted more than spatial structure and diversity. The TRT viability report did not include uncertainty in the attribute weights and this is a new feature of this analysis.

If the overall population summary is based on the abundance and productivity rating because it is lower than the spatial structure and diversity ratings, a different method for describing the overall population diamond is applied. The diamond graphs are a representation of a triangular distribution, which is define by three parameters: 1) mode, 2) lower bound, 3) upper bound. The mode is the point estimate or "most likely" value and is the fattest part of the diamond. If, after applying the rule above, the abundance and productivity mode will be used as the overall population mode, the lower and upper bounds on the overall population summary diamond are determined as the minimum lower or upper bound of all three attributes (Equations 3 and 4).

$$\text{Equation 3: popLower=min(A\&P\_Lower, SS\_Lower, DV\_Lower)}$$

$$\text{Equation 4: popUpper=min(A\&P\_Upper, SS\_Upper, DV\_Upper)}$$

This sets the most precautionary upper and lower bound for the overall population diamond considering all the population attributes.

The overall population status is presented in the form of the diamond graphs and we do not present the results in a "pass" or "fail" format. We prefer the diamond graph method because it retains more information (i.e., the uncertainty inherent in the analysis). If a pass or fail decision is required for a management decision, it is important that that decision be made with an understanding of the full range of possible risk status for the populations. By presenting the results as a distribution of possible extinction risks, the results of this analysis may be applied to different sorts of management problems, which may require different levels of precaution regarding risk.
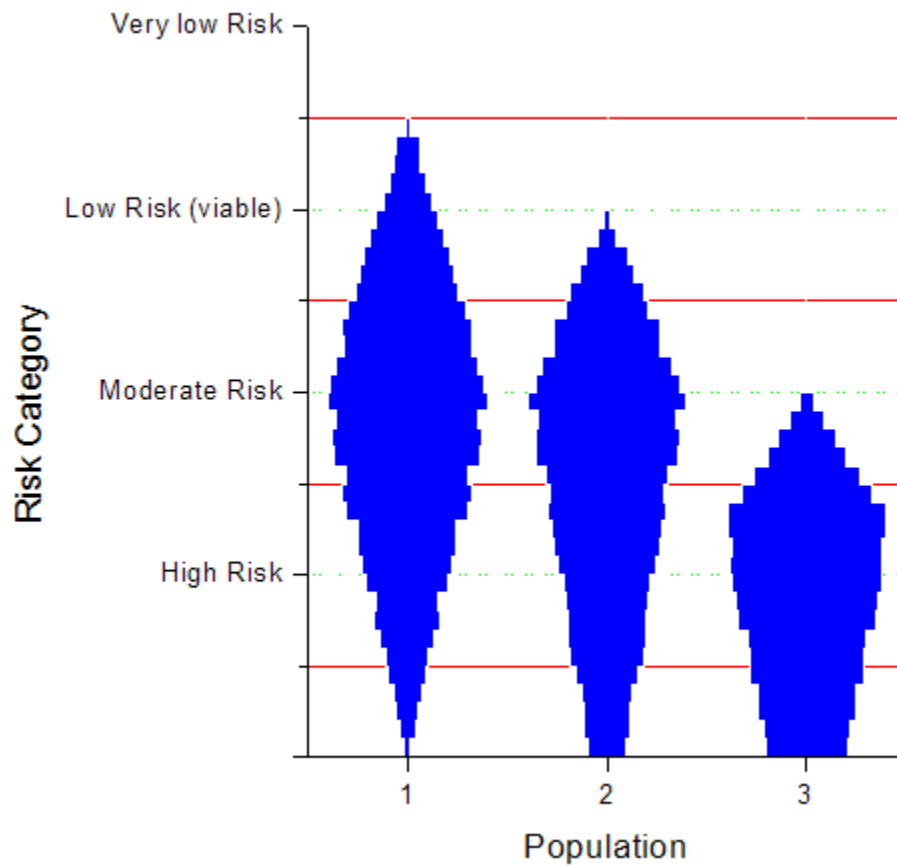
Figure 1: Example risk summary "diamond graph" for three populations with different risk profiles. The risk categories correspond to the probabilities in Table 1.

Abundance and Productivity

The abundance and productivity evaluation is predicated on two basic observations: 1) all else being equal, a larger population is less likely to go extinct than a small one and 2) all else being equal, a highly productive population is less likely to go extinct than a population with low productivity. Productivity is an indication of a population's "resilience" or tendency to return to high abundance if perturbed to low abundance. We typically measure productivity as the number of offspring per parent when there are very few parents (in fisheries parlance, "intrinsic productivity" or "recruits per spawner at extremely low spawner densities").

The quantity and quality of data available to evaluate the abundance and productivity varies dramatically among WLC populations. We can divide the populations into two basic groups: those with sufficient time series of abundance and related parameters for a quantitative evaluation and those without sufficient time series. For those with a time series, we explored a number of analytical approaches which are described in more detail below and in the viability report. For those without an adequate time series, we examined any available information (e.g., one-time surveys, qualitative reports) and often had to rely on extrapolation from assessments of similar populations where quantitative analysis was possible. Even for populations where a time series was available, we did not limit our analysis to the metrics described below, but examined any relevant piece of information. Time series used for the viability analysis are included in this report as Appendices B and C. For populations with adequate time series data, we present some general summary statistics, including comparison to a simple minimum abundance threshold, plus the results of three Population Viability Analysis (PVA) modeling approaches: 1) Viability Curve Criteria (VCC), 2) the Conservation Assessment and Planning Model (CAPM) and 3) a simple generic stochastic stock recruitment model (PopCycle). By exploring three different extinction risk models, we can develop better extinction risk estimate and understanding of the confidence around that estimate.

Summary Graphics and Statistics

Simply viewing a few summary graphs, like the abundance time series and a few simple statistics like the fraction of hatchery origin spawners can provide a lot of information for the abundance and productivity evaluation. For each population with adequate data, we present graphs of the time series of spawner abundance (distinguishing between total spawners and natural origin spawners), the time series of the fraction of hatchery origin spawners, the time series of harvest rate, and both escapement and pre-harvest recruitment curves. A table of summary statistics was also generated, showing the time period of the series, average abundance, average recruitment, growth rates, etc. Descriptions of the statistics estimated for every population with an available time series are shown in Table 2. These statistics were calculated for two different time periods: 1) the length of the entire available time series (which differs by population); and 2) the time series from 1990 to the most currently available year (typically 2004 or 2005). The 1990-current period is arbitrarily described as "recent". Where appropriate, statistics are also estimated based on both escapement and pre-harvest recruitment, since both sorts of calculations provide information for extinction risk analysis. In these analyses, the relative reproductive success of hatchery origin spawners is assumed to be the same as

natural origin spawners (see viability report for a discussion of this issue). Many of the metrics presented in this summary table are likely to be highly correlated (e.g. Lambda and trend in ln(abundance)), and it would be reasonable to reduce the number of metrics to eliminate redundancy and shorten the table. However, all of these different metrics have been used in the past in different salmon assessments and we considered it useful to include all the metrics for comparative purposes.

Tables of the recruitment curve fits are also provided for both the escapement and preharvest analyses, where data were available. We estimated productivity, capacity and recruitment variance for the random walk, random walk with trend, constant recruitment, hockey-stick, Beaverton-Holt, Ricker, and MeanRS recruitment functions. The MeanRS recruitment function is described in the section below on viability curves. Equations for the other models are shown in Table 3. For all models except the MeanRS, parameters were fit using a Bayesian approach and we provide both point estimates and 95% posterior probability intervals. For the MeanRS method the 95% intervals were based on a bootstrap of 10,000 resamplings with replacement. We also present relative corrected Akaike information criterion (AICc) values to compare the 'fit' of the alternative models (Burnham and Anderson 1998). The model that is the "best" approximation has a relative AICc = 0. Models that are nearly indistinguishable from best have a relative AICc <2. Models that are possible, but less likely, contenders as best have 2 < relative AICc < 10. Models that are very unlikely to be the best approximating model have relative AICc > 10.

Table 2: Description of abundance and productivity statistics calculated for populations with abundance time series.

Statistic	Description
Time Series Period	Years used in the analysis
Length of Time Period	Number of Years used in the analysis
Geometric Mean Natural Origin Spawner Abundance	Geometric mean of natural origin spawners with 95% confidence intervals shown in parentheses. This parameter is compared to the minimum abundance threshold MAT and colored blue, green, orange, yellow or red for the very low risk, low risk, moderate risk, high risk or very high risk categories, respectively (see Figure 2)
Geometric Mean of Recruit Abundance	Geometric mean of natural origin recruits (either to escapement or pre-harvest) with 95% confidence intervals shown in parentheses. If recruits to escapement, will be similar, but not identical to geomean natural origin spawners. The geometric mean recruits is the "**Abundance**" parameter of the MeanRS method viability curve.
Lambda	Median annual population growth rate based on four-year running sum with 95% confidence interval. The variance estimate used to estimate the confidence interval uses the slope method approach of Holmes (2000). The statistic is the same used in recent NOAA status evaluations (Good et al.) Values above one indicate a growing population, values below one indicate a declining population. The statistic is corrected to hatchery fish to show the growth rate of the natural population if there had not been a hatchery subsidy.
Trend in Natural Origin Abundance	This is the exponentiated slope of the regression of ln(natural origin spawners) vs. year. The 95% confidence intervals are shown in

	parentheses. Values above one indicate an increasing number of natural origin spawners; values below one indicate a declining number of natural origin spawners. Hatchery origin spawners are ignored in the estimation of this statistic.
Geometric Mean Recruits per Spawner	Geometric mean of recruits per spawner using all brood years in the analysis period. The 95% confidence intervals are shown in parentheses.
Geometric Mean Recruits per Spawner for Broods below Median	Geometric mean of recruits per spawner using brood years where the spawner abundance is less than the median spawner abundance. The idea is to estimate recruits per spawner under conditions with reduced dependent effects. The 95% confidence intervals are shown in parentheses. This is the "**Productivity**" parameter of the MeanRS method viability curve.
Average Hatchery Fraction	The arithmetic average fraction of hatchery origin spawners on the spawning grounds over the time series period.
Average Harvest Rate	The arithmetic average harvest rate of natural origin fish over the time series period.
CAPM frequency distribution of estimated extinction probabilities	Median extinction probability for each population derived from 200 bootstrap samples of the raw data set. Included (in parentheses) are values for 5th and 95th percentiles associated with the median probability (50th percentile). This value is explained in more detail in the section on the CAPM model and in Appendix E.
PopCycle extinction risk estimate	This is the population extinction risk result from the PopCycle model as describe in the PopCycle section below and in Appendix F.

Table 3: Recruitment functions used for summary analysis of Oregon WLC salmon and steelhead populations.

Model Name	Equation [a]
Random walk	$R = S \exp(\sigma_0 Z)$
Random walk with drift; stochastic exponential growth or decline	$R = S \exp(a_1 + \sigma_1 Z)$
Constant recruitment	$R = b_2 \exp(\sigma_2 Z)$
Stochastic hockey stick; stochastic exponential growth with a ceiling	$R = \min(S, b_3) \exp(a_3 + \sigma_3 Z)$
Ricker; stochastic logistic	$R = S \exp(a_4 + b_4 S + \sigma_4 Z)$
Beverton-Holt	$R = \dfrac{a_5 S}{1 + \dfrac{a_5}{b_5} S} \exp(\sigma_5 Z)$

[a] In the equations,

S_t = the number of spawners

R = the number of recruits

Z = a unit normal random variable

$\sigma_\#$ = the standard deviation of the process error

$a_\#$ and $b_\#$ = equation-specific parameters, with the $a_\#$ parameter relating in some way to "intrinsic productivity" and the $b_\#$ parameter relating in some way to "capacity"

Population Size Thresholds

The TRT viability report describes population minimum abundance thresholds (MATs) as one part of the abundance and productivity evaluation. Before placed in a particular risk category, a population should exceed the MAT criterion AND exceed the viability curve criteria (described below) AND exceed any of the TRT's qualitative criteria for that category. The MAT criteria are derived from a combination of general conservation biology literature recommendations and the results of the viability curve analysis. These thresholds apply to the estimated long-term geometric mean natural origin spawner abundance, and the viability report indicates that the threshold should meet with a reasonable level of confidence.

The viability report does not provide specifics on either "long term" or "reasonable," but suggests that at least 12 years of data are required and that simply observing a point estimate above a given threshold is not sufficient (i.e., the metric should be some statistical confidence limit.) The thresholds used in this analysis are presented in Figure 2 and Table 4. These thresholds differ from the thresholds presented in the viability report because newer estimates of population variability based on inclusion of additional data from Washington suggested a revision of the thresholds (see Appendix D). MAT evaluations are included in the population summary tables using a simple color coding as described in Table 2.
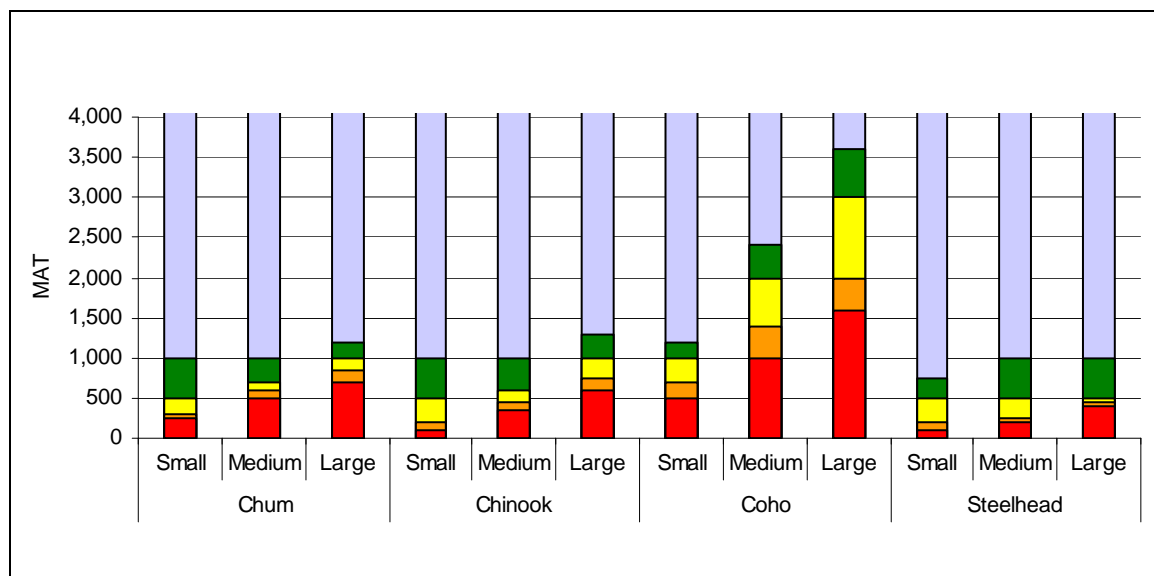
Figure 2: Abundance thresholds for population persistence categories by species and watershed size. The red, orange, yellow, green and blue bars show the ranges for persistence categories 0, 1, 2, 3, and 4, respectively. Figure data are shown in Table 4.

Table 4: Population abundance relative to persistence category. Data are graphed in Figure 2.

Species	Size Category	Persistence Category				
		0	**1**	**2**	**3**	**4**
Chum	Small	<250	250-300	300-500	500-1,000	>1,000
	Medium	<500	500-600	600-700	700-1,000	>1,000
	Large	<700	700-850	850-1,000	1,000-1,200	>1,200
Chinook	Small	<100	100-200	200-500	500-1,000	>1,000

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	Medium	<350	350-450	450-600	600-1,000	>1,000
	Large	<600	600-750	750-1,000	1,000-1,300	>1,300
Coho	Small	<500	500-700	700-1,000	1,000-1,200	>1,200
	Medium	<1,000	1,000-1,400	1,400-2,000	2,000-2,400	<2,400
	Large	<1,600	1,600-2,000	2,000-3,000	3,000-3,600	>3,600
Steelhead	Small	<100	100-200	200-500	500-750	>750
	Medium	<200	200-250	250-500	500-1,000	>1,000
	Large	<400	400-450	450-500	500-1,000	>1,000

Viability Curves

This section contains a brief description of viability curve analysis, with a more detailed description available in the TRT viability report (McElhany et al. 2006a). Appendix D describes some modifications to TRT report viability curve methodology that apply to this status evaluation. The viability curve approach developed out of efforts to establish recovery criteria for threatened salmon and steelhead populations and was first described in McElhany et al. (2003). A viability curve describes a relationship between population abundance, productivity and extinction risk, with all the points on the curve showing abundance and productivity combinations that generate the same risk (Figure 3). Populations with productivity and abundance combinations above (to the right) of the viability curve have a lower extinction risk than that of the curve, while those below (to the left) have a higher risk.

Relating abundance, productivity and extinction risk is accomplished using a simulation model with a stochastic hockey-stick recruitment function having terms for productivity, carrying capacity, recruitment variability, age structure, future harvest rate, and a reproductive failure threshold (RFT). To estimate extinction risk for any particular set of input parameters, we run the model thousands of times and look at the fraction of simulations that drop below a critical risk threshold (CRT[3]). To draw the curve, we look for combinations of productivity and capacity (abundance) that are associated with a given level of risk. Drawing the curve for any particular group of fish requires appropriate estimates of recruitment variability, age structure, future harvest rate, and RFT. Note that we do not estimate productivity and capacity to draw the curve – in the curve we explore a range of hypothetical abundances and capacities (abundances). The viability curve can be thought of as a target for population abundance and productivity. The viability curve itself is not a complete evaluation of population status.

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[3] The term 'critical risk threshold' (CRT) replaces the viability report term of 'quasi-extinction threshold' (QET) as described in Appendix D.
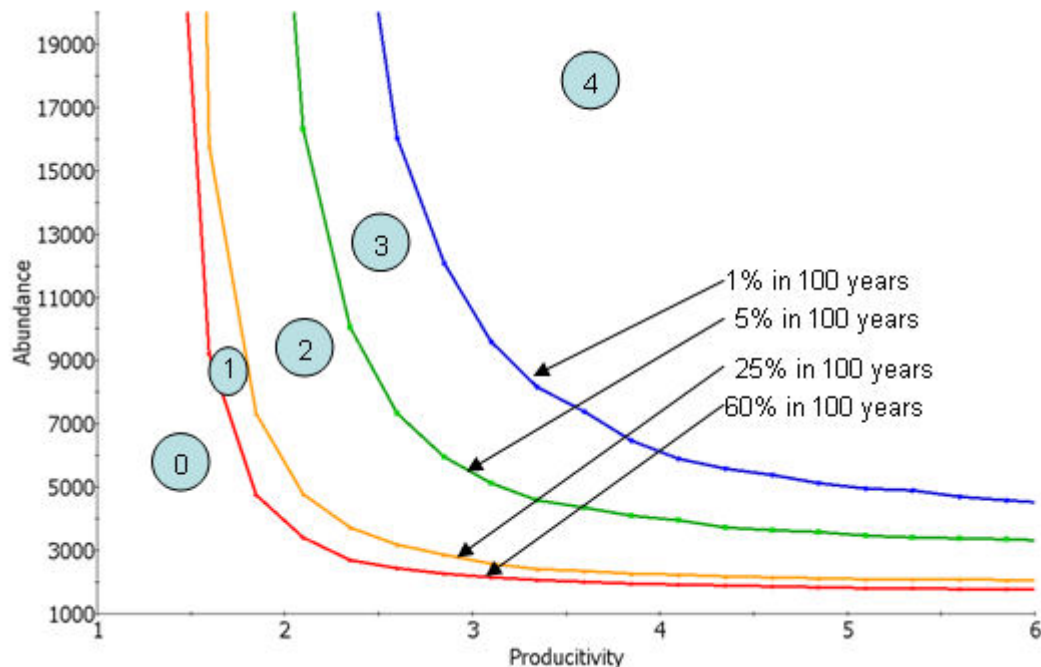
Figure 3: Viability curves showing relationship between risk levels and population persistence categories (example based on chinook curve). Each of the curves indicates a different risk level. The numbers in circles are the persistence categories associated with each region of the chart (i.e., the area between the curves). A population with a risk category 0 is described as a population that is nearly extinct and population with a risk category of 3 is described as "viable" (see Table 1).

In order to evaluate where any particular population is relative to the viability curve target, we must estimate the population's abundance and productivity. We used the MeanRS method described in the TRT viability report to estimate these parameters. Productivity is a measure of a population's resilience or tendency to return to higher abundance if the population declines to low abundance. Using the MeanRS method, this tendency is estimated as the geometric mean recruits per spawner for the brood years with the lowest half of spawner abundances. The abundance is estimated as the geometric mean recruitment over the time series. The characteristics of the MeanRS method compared other possible approaches are described in the viability report. The MeanRS methods are solidly based on the empirical data because they do not depend on extrapolation outside the observe ranges of recruitment and abundance.

Estimating a population's abundance and productivity requires input data on population spawner abundance, the fraction of hatchery origin spawners, harvest rates and the population age structure. All of these parameters are estimated with error – sometimes considerable error. We incorporate information about that error into our analysis by using a Monte Carlo approach of simulating many equally plausible data sets based on our understanding of the measurement errors and then calculating the MeanRS output for each simulated data set. This gives a distribution of possible abundance and productivity combinations for the current state of the population, which we present in the form of probability contours (a.k.a. "blobs") (Figure 4). We used the Salmon Population AnalyZer (SPAZ) computer program to generate viability curves and the current status distribution contours (McElhany et al. 2006b).
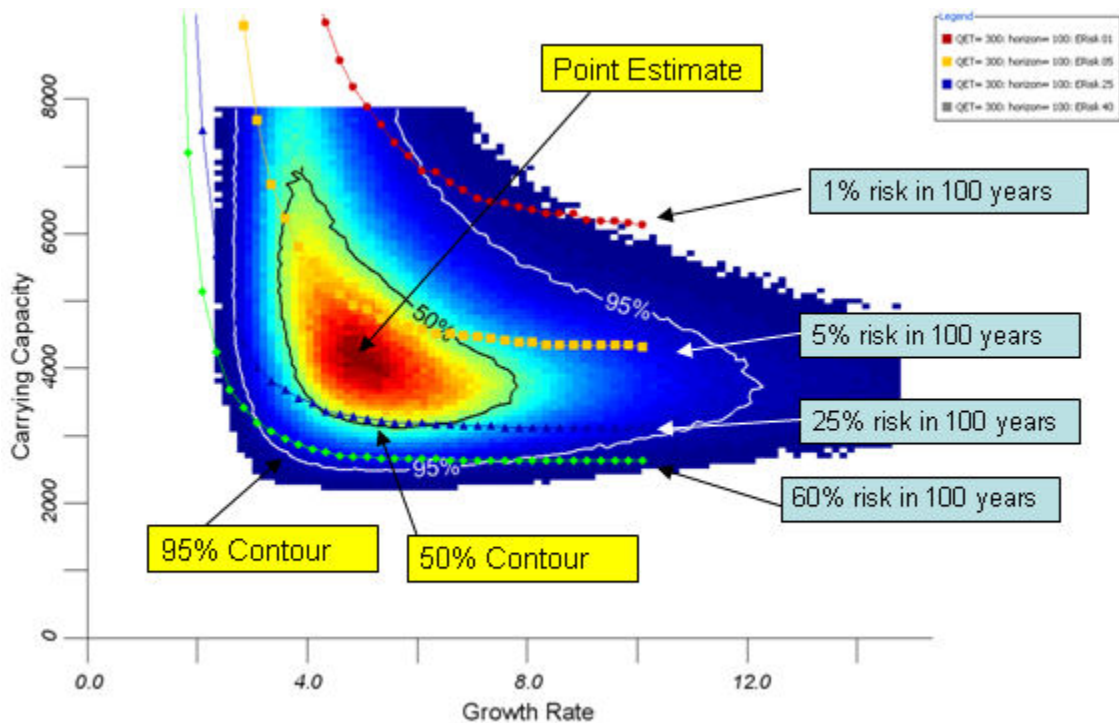
Figure 4: Example of current status contours combined with viability curves. In this example, the point estimate of the population indicates a persistence category of 2 (i.e., between 25% and 5% viability curves). To ensure at least a 50% chance that the population exceeds a given viability curve we would examine the 50% contour, which in this example suggests the population is in persistence category 1 (the bottom of the 50% contour is between the 40% and 25% viability curves).

CAPM Viability Model

Where appropriate time series were available, we also analyzed population viability using an extinction risk model that makes explicit use of information available over the recent past. This model, CAPM (Conservation Assessment and Planning Model) and its interpretation are described in Appendix E. A summary is provided here.

CAPM is a population viability model developed to assist salmonid conservation and recovery planning in Oregon. With the ability to define a wide range of possible future conditions the model lends itself to assessing both the likelihood of population extinction should conditions remain unchanged and also the likelihood of population extinction should these conditions change in response to implementation of successful recovery strategies. As is characteristic of all viability models, CAPM attempts to mimic the stochastic nature of population recruitment for a future period of time (e.g., the next 100 years). Simulations of this natural process are the basis for estimating probabilities of extinction, or in this case abundance less than CRT.

Although mechanically similar to other population viability models, several features of CAPM are unique. First, rather than using only one recruitment model to simulate population recruitment, CAPM uses three. It was assumed that in doing so, the adverse consequences of case-by-case inaccuracies of data fits to a particular recruitment function could be reduced. Secondly, in addition to the spawner abundance variable, all

recruitment equations incorporate an independent index of environmental conditions. This second variable, called SNEG, was based on a 7-year moving average of high elevation maximum snow depth (see Appendix E). Inclusion of this variable not only improved recruitment model accuracy, but also had the effect of substantially reducing temporal autocorrelation of recruitment model residuals.

Another unique feature was that a probability of extinction was calculated for each set of recruitment function parameters estimated via the bootstrap process. This bootstrapping procedure was used to repeatedly sample each population data set (generally 200 times). A regression analysis was then performed on each data set sample using a nonlinear regression routine. This meant that for every bootstrap sample an estimate of recruitment equation parameters and associated standard deviations were generated for all three recruitment curves. Probabilities of the population becoming less than CRT levels were then estimated for each sample of parameters. The primary purpose of this extended bootstrap procedure was to better understand the range and magnitude of possible errors in estimating recruitment equation parameters. However, as a result of this process, the outputs from CAPM are not a single probability of CRT estimates, but rather distributions of CRT probabilities that can be visualized as frequency histograms. The median and percentile values from these distributions are used to characterize the population viability.

PopCycle Stochastic Stock-Recruitment Model

Oregon WLC populations were also evaluated using a generic risk analysis model (Popcycle) developed for application to Washington lower Columbia River salmon populations and fisheries. The model is described in more detail in Appendix F, but a brief summary is provided here. Popcycle is a simple stochastic stock-recruitment population model that projects annual run size, spawning escapement, and harvest numbers and frequency distributions based on user-defined population functions and parameter values. A simple interface page facilitates model use and review of results. The model includes optional inputs to apply fishing rates in each year to calculate harvest and fishery effects on population dynamics. Optional inputs are also included for analysis of demographic effects of natural spawning by hatchery fish based on inputs for hatchery releases, release to adult survival, and rates of natural spawning by hatchery fish. The model is built in Microsoft Excel using Visual Basic. In contrast to the viability curve and CAPM viability curve analyses, PopCycle estimates only expected averages and frequency distributions, and does use parameter uncertainty estimates to estimate confidence or plausibility regions about expected results. However, the simpler model formulation and ease of use of PopCycle facilitates exploration of population dynamics and model sensitivity to differences in population parameters and key assumptions.
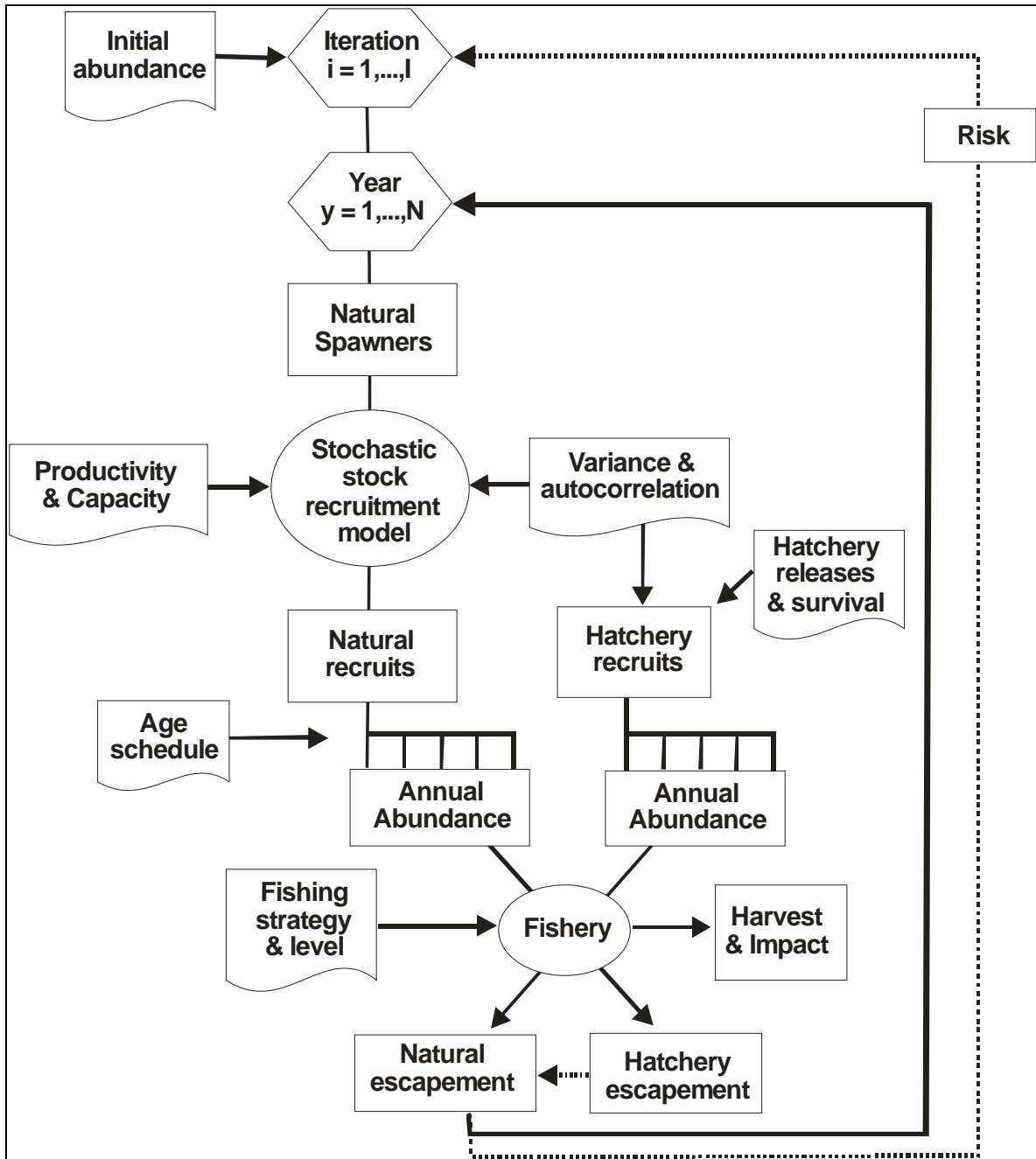
Figure 5: PopCycle model algorithm.

Viability Curve and CAPM Model Summary Table

A summary table from the viability curve, CAPM, and PopCycle analyses is provided for each population that had adequate data. This table provides estimates of the probability that the population is in each of the persistence categories. As is common with all extinction risk forecasts, the accuracy of these probability assessments depends upon the validity of the underlying model assumptions. For the viability curve analysis this statistic is estimated by integrating the fraction of the probability contour above a given viability curve. For example, if we are looking at a 5% extinction risk in 100 year

viability curve and if the probability contour ("blob") for a population is completely below the curve, the probability that the risk is less than 5% in 100 years is zero. Conversely, if the probability contour is completely above the curve, the probability that the risk is less than 5% in 100 years is 1. If the viability curve goes through the probability contour, there is some probability between zero and one that the risk is less than 5% in 100 years; the more of the contour above the curve, the closer to one. This gives a measure of how sure we are that the population is above a given risk threshold and is a quantification of the visual assessment of what fraction of the probability contour lies above a given viability curve. For the CAPM model, the probability that the population is above a given threshold is calculated as described in Appendix E.

Combining Abundance and Productivity Information

Combining information from the various summary statistics and extinction risk models was done using professional judgment rather than a quantitative algorithm. In general, all the information points to a similar conclusion about population status, so the overall result is fairly obvious. However, in some cases, the different analyses suggest different conclusions. In these cases, we discussed the alternative interpretations and generally indicate the increased ambiguity about the population's status by increasing the amount of uncertainty displayed in the diamond figures used to show conclusions on population status.

Spatial Structure

Overview

Spatial structure of Oregon populations was assessed based on the application of basic principles and a coho example developed by the TRT (McElhany et al 2006a). Quantitative metrics address two of the key spatial structure issues: 1) total quantity of available habitat and 2) spatial distribution of accessible habitat. In addition, quantitative scores were adjusted based on qualitative considerations including habitat quality and life-stage specific spatial distribution. Adjustments are discussed in the text narrative for each population.

Spatial structure evaluations were primarily based on the evaluation of maps of accessible habitat developed in the Oregon WLC habitat atlas (Maher et al. 2005). These maps have some important limitations. They were developed using existing blockage databases and species-specific gradient thresholds. There is no consideration of habitat quality; the maps simply provide an estimate of where fish could go, not necessarily where the habitat can support fish or where fish currently are. Consequently, the maps likely overestimate current and historical use, perhaps substantially (see habitat atlas for discussion and comparison to potential use maps). The maps are also only as good as the blockage databases, which may contain some errors. In addition, the maps only address adult accessibility; they do not describe life stage specific habitat spatial distribution, such as the arrangement of habitat for juvenile rearing. Despite these caveats, the maps can provide useful information and as they where developed using a consistent protocol comparing current and historical potential distribution for the entire ESU/DPS, we have based the analyses on the maps. However, we do not rely solely on these maps and incorporate additional information in the final spatial structure evaluations. The refinement of maps describing current and historical habitat from a fish perspective should be a research priority.

Quantitative Metrics

A primary concern in evaluating spatial structure is whether the population has access to a sufficient quantity of habitat to survive catastrophic events. A viable population should not "put all its eggs in one basket." The TRT developed metric and threshold guidelines that are a function of both the amount of historically accessible habitat and the size of the watershed (Table 5). These thresholds are used in this current status evaluation. Historical accessibility is considered the appropriate reference value because the historic structure was assumed to be viable and the greater the deviation from the historical condition, the greater the risk. The guideline thresholds are a function of the watershed size because a smaller population is likely to be at a greater risk from a smaller relative loss than a larger population. These guidelines are not based on any quantitative model, but rather on the professional judgment of the TRT. The TRT included quantitative guidelines, not because they believed there is any quantitative precision in this assessment, but instead to provide a transparent presentation of how they view the relationship between the loss of habitat access and extinction risk.

Table 5: Guideline thresholds for relationship between persistence category and percent loss in accessible habitat.

Persistence Category	Watershed Size		
	Small	Medium	Large
0	50-100	60-100	75-100
1	25-50	40-60	50-75
2	15-25	20-40	25-50
3	5-15	10-20	15-25
4	0-5	0-10	0-15

Another key consideration is the spatial distribution of habitat loss. The TRT hypothesized that loss of access to an entire stream branch poses a greater risk to a population than a number of smaller losses that would produce the same total amount loss. The relative size of a stream branch loss can be evaluated as the percent of loss caused by each blockage. We apply the following guideline from the TRT viability report:

> If the largest single blockage results in a >10% loss for small watersheds or a >15% loss for medium and large watersheds, the persistence category is reduced by 0.5.

For example, a persistence category 3 would become a 2.5. This metric addresses some of the aspects of the arrangement of the loss in space, but is not a complete evaluation. The natural dendritic structure or "branchiness" of a stream and the exact location of the blockage can also be important. This aspect of spatial structure is difficult to quantify and set a priori thresholds. Therefore, we applied a qualitative evaluation based on consideration of the actual access maps.

Qualitative Spatial Considerations

In addition to the two spatial structure metrics described above, we applied adjustments to the scores based on qualitative considerations, which are discussed in the text narrative for each population. Qualitative factors considered are habitat quality and life-stage specific spatial distribution.

Diversity

The diversity evaluation follows the basic methods and approach of the viability report (McElhany et al. 2006a). However, the evaluation is organized slightly differently, with analyses divided into the following factors:

- Life history traits
- Effective population size
- Impact of Hatchery Fish
- Anthropogenic mortality
- Habitat diversity

Where data are available, we evaluate and assign a persistence score for each of these five diversity factors. These scores are then combined into a single diversity rating for each population. The overall diversity persistence score is estimated using expert judgment and considering all the individual diversity factor scores (i.e., there is no quantitative algorithm for combining the diversity factors). It should be noted that data are frequently insufficient to adequately evaluate one or more of the diversity factors.

Life History Traits

Measurable life history traits considered in our analyses include: 1) timing of return to fresh water, 2) age at maturation, 3) spawn timing, 4) outmigration timing, 5) smoltification timing, 6) developmental rate, 7) egg size, 8) fecundity, 9) freshwater distribution, 10) ocean distribution, 11) size at maturation and 12) timing of ascension to the natal stream. To assigned persistence scores for life history traits we generally relied on the risk guidelines developed by the Interior Columbia TRT (IC-TRT 2005)and modified by the WLC-TRT (McElhany et al. 2006a) (Table 6).

Table 6: Preliminary criteria describing risk levels associated with major life history strategies and change in phenotypic characteristics (from ICRTRT 2005).

Factor	Risk Level (Viability Score)			
	Very Low (4)	**Low (3)**	**Moderate (2)**	**High (1)**
Distribution of major life history strategies within a population.	No evidence of loss in variability or change in relative distribution	All historical pathways present, but variability in one reduce or relative distributions shifted slightly.	All historical pathways present, but significant reduction in variability or substantial change in relative distribution.	Permanent loss of major pathway.
Reduction in trait variability of traits, shift in mean value of trait, loss of traits	No evidence of loss, reduced variability, or change in any trait.	Evidence of change in mean or variability in 1 trait.	Loss of 1 trait or evidence of change in mean and variability of 2 or more traits.	Loss of 1 or more traits and evidence of change in mean and variability of 2 or more traits.

Effective Population Size

One of the indirect measures of diversity is effective population size. A population at chronic low abundance or experiencing even a single episode of low abundance can be at higher extinction risk because of loss of genetic variability, inbreeding and the expression of inbreeding depression, or the effects of mutation accumulation. The viability report identifies increased risk as significant when the effective population size drops below about 500. The relationship between effective population size, census population size, and estimated persistence category are shown in Table 7.

Table 7: Relationship between effective population size, census population size (in parentheses) and estimated persistence category. From (McElhany et al. 2006a).

Effective Population Size	Persistence Category				
	0	1	2	3	4
$N_e < 12.5$ (*N<25*)	x				
$12.5 < N_e < 25$ (*25<N<50*)		x			
$25 < N_e < 125$ (*50<N<250*)			x		
$125 < N_e < 500$ (*250<N<1000*)				x	
$500 < N_e$ (*1000<N*)					x

Impact of Hatchery Fish

Interbreeding of wild populations and hatchery origin fish can be a significant risk factor to the diversity of wild populations because of the potential genetic dissimilarities between these two groups of fish. We evaluate this risk based on two characteristics of the problem, the proportion of hatchery fish within the natural spawning population and the genetic similarity of these hatchery fish to the wild population. Our assumption is that the genetic risk to the wild population is greatest when the proportion of hatchery fish in the spawning population is high and their genetic similarity to the wild population is low. Conversely, the lowest risk occurs when the proportion of hatchery fish is low and they are genetically similar to the wild population.

We use three different methods to evaluate the potential impact of hatchery fish: 1) Proportion of Natural Influence (PNI) modeling for domestication in integrated hatchery programs; 2) Thresholds for introgression with out-of-stratum hatchery broodstocks; and 3) Synthetic approach based on fraction of hatchery origin spawners.

Domestication PNI Modeling
For interactions with locally derived hatchery brood stocks, we considered the hatchery and natural spawners as part of a potential "integrated" population. The approach to assessing risk is based on evaluating the Proportion of Natural Influence (PNI) index, a measure of potential domestication. The index is the ratio of the proportion of natural origin fish in the hatchery brood stock and the proportion of hatchery origin fish on the natural spawning grounds (Figure 6). The lower the PNI, the greater the population risk from domestication, because the majority of the breading takes place in the hatchery. Following the viability report, we related the PNI to potential fitness loss (Figure 7) and associated the fitness loss with a population persistence category (Table 8). As a precautionary measure the fitness loss measure is based on the *lower* confidence bound. In many cases hatcheries are run as "isolated" programs with no known inclusion of naturally-produced spawners into the hatchery broodstock, although there is generally some straying of hatchery origin fish onto the natural spawning grounds. Isolating the

hatchery broodstock produces a PNI of 0, regardless of the proportion of hatchery fish on the natural spawning grounds. In these situations, the PNI approach is not applicable, and we rely on the other two methods for evaluating hatchery impacts on diversity.

The PNI model was developed to estimate the potential decline in fitness due to selection for hatchery conditions rather than natural conditions (aka domestication) and does not directly address the other possible consequences of hatchery/wild interaction. Domestication effects were modeled using empirical estimates from studies and estimates based on the professional opinion of a number of fisheries scientists. As such, the PNI model represents a work in progress and it is likely that further refinements will be made as more information on hatchery effects becomes available. While the focus was on "domestication" it is likely that non-domestication effects were incorporated into estimates of decline in fitness. Other effects include competition, predation, non-genetic domestication (behavioral and developmental), disease, etc. The impacts of these effects will generally be reflected in the assessment of population productivity, which integrates all factors affecting mortality. However, the PNI metric does provide some information on these factors, since the hatchery effects are largely a function of the fraction of hatchery origin fish on the spawning grounds, which is one factor in the PNI metric. We present information on how the domestication thresholds relate to the fraction of hatchery origin fish in Table 8. Often, populations with hatchery fish will show poor productivity estimates at hatchery fractions lower than those that cause significant domestication effects because of how hatchery fish enter the productivity equations (i.e., hatchery fish on the spawning grounds count as spawners, but not natural origin recruits.).
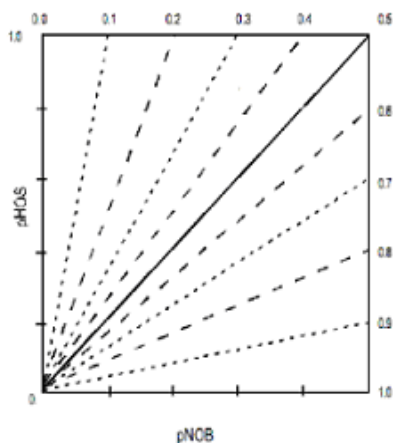
Figure 6: Proportion of Natural Influence (PNI) relationship between percent Hatchery Origin Spawners (pHOS) and percent Natural Origin Broodstock (pNOB). The numbers are the outside of the graphic represent the PNI score. Populations located toward the lower right corner are at relatively lower risk of domestication and populations located toward the upper left corner are at relatively higher risk.
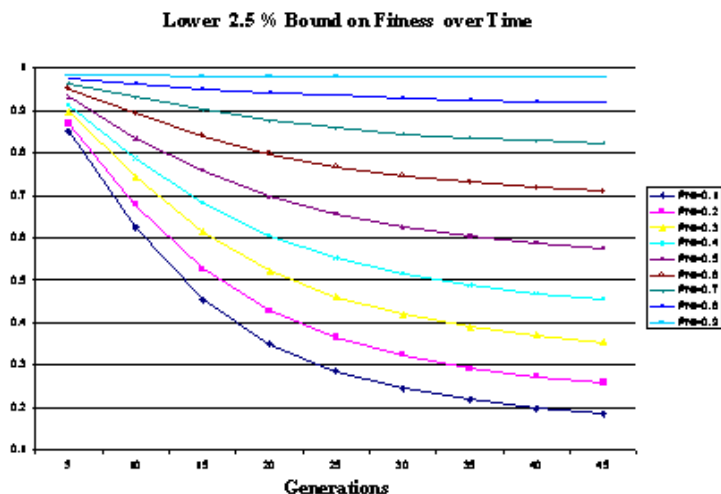
Figure 7: Influence of PNI on overall population fitness over time (generations). Fitness estimates are based on the lower 2.5% bound of the confidence intervals. (Graphic from C. Busack, WDFW)

Table 8: Loss of fitness over time (from Figure 7) and diversity score for populations affected by artificial propagation programs.

Percent Fitness Loss	Diversity Score	PNI at 25 generations	pHOS at 50% pNOB
0.0 -2.5	4	0.9	10%
2.5 – 5.0	3.5	0.85	15%
5.0 – 10.0	3.0	0.8	20%
10.0 – 15.0	2.5	0.7	30%
15.0 – 25.0	2.0	0.6	40%
25.0 – 45.0	1.5	0.5	50%
45.0 – 65.0	1.0	0.4	60%
65.0 – 85.0	0.5	0.3	70%
> 85.0	0	0.1	90%

Introgression Thresholds for Out of Stratum Stocks

If there is interbreeding between a natural population and hatchery or wild stocks from outside the stratum, the effects are not as easily estimated by the PNI/Hatchery Domestication approach. The genomes of the populations are likely to have differences not caused solely by domestication to the hatchery environment, but will also exhibit differences from local adaptation to other basins. We are concerned in this risk factor not just about hatchery fish from outside the stratum but also artificially high interbreeding with natural origin fish from outside the stratum. Although some interbreeding of fish from different strata occurs naturally, some human activities (like altering passage at Willamette Falls) can create elevated levels of interbreeding. The potential for reduced viability is greater for out of ESU/DPS interbreeding than for out of stratum, but within ESU/DPS, interbreeding. The relationship between stray rates and risk categories is shown in Table 9 (from McElhany et al. 2006a). The hatchery introgression tables are also used in situations where a local hatchery is operated as an isolated program—without the inclusion of naturally-produced fish into the broodstock. In these situations the PNI metric always produces a PNI value of zero, regardless of the hatchery stray rate onto the natural spawning grounds.

Table 9: Influence of non-local origin fish strays on the diversity status of the local population. For the diversity metric, strays are only considered if there is evidence of interbreeding, the effective stray rate. Where both within ESU and out-of-ESU strays are present, a weighted mean (using the proportional occurrence of both types of strays) should be calculated.

Diversity Score	0	1	2	3	4
Within ESU/Out of Strata Effective Stray Rate (m)[1]					
75% < m	x				
30% < m < 75%		x			
10% < m < 30%			x		
5% < m < 10%				x	
m < 5%					x
Out of ESU Effective Stray Rate (m)[1]					
50% < m	x				
20% < m < 50%		x			
5% < m < 20%			x		
2% < m < 5%				x	
m < 2%					x

For example, if 10% of the natural spawners in a basin were from a different strata within the ESU, and 5% were from outside of the ESU, the stray metric would be calculated as:

(.67) * (2 [w/i ESU@20%]) + (.33) * (3 [out of ESU@10%]) = 2.3.

Remember that the stray rate is based on the proportion of effective (spawning) non-local fish.

Synthetic Approach

The synthetic approach considers both domestication from integrated programs and introgression from out of strata fish within a single framework based on the proportion of hatchery origin spawners (Ph). This method was developed for this report to provide a streamlined metric based on empirical estimates of hatchery fish induced productivity declines (Chilocte 2003), rather than modeling genetic processes (i.e. PNI). To formulize the relationship between proportion of hatchery spawners and a persistence score we have adopted a modified version of the rating system in Table 9. This rating system differs from Table 9 in two important ways. First, rather than specifying an effective migration rate (m), the approach here is based on the proportion of hatchery origin spawners within the basin shared by wild fish. No distinction is made for spatial or temporal segregation of hatchery and wild spawners, only presence is counted. This is an adjustment based on the reality that in most cases it is exceedingly difficult to measure effective migration rate (m). In contrast, Ph can be determined easily if a means to discriminate between hatchery and wild fish is available and the data are collected.

Secondly, the rating assumes the baseline hatchery stock has a low genetic similarity to the local wild population. However, if evidence suggests a moderate to high similarity between the hatchery and wild fish, then the persistence score is incremented by one. In contrast, if the hatchery stocks involved likely have a very low genetic similarity to the wild population, a decrement of one persistence score category is applied. A matrix display of this rating system is presented in Table 10.

The classification of the hatchery stocks into one of three similarity categories was made largely on the basis of broodstock origin and incorporation of wild fish into the hatchery spawning cycle. Where possible, genetic analysis of hatchery and wild populations was examined to estimate the degree of similarity. The 'very low' genetic similarity

classification was reserved for those hatchery stocks whose origin was from outside of the stratum or the ESU. The 'low' classification was assigned to the hatchery stock if its origin was within the same stratum. The 'moderate' classification was used for those hatchery stocks that were derived from the local wild population and for which more than 50% of the spawners used to each generation for hatchery broodstock were wild fish.

Table 10: Persistence scores for different proportions of hatchery fish within naturally spawning populations of mixed hatchery and wild fish.

Presumed Genetic Similarity to Wild Population	Proportion of Hatchery Fish (Ph) in Natural Spawning Population	Persistence Score				
		0	1	2	3	4
Moderate (Broodstock from same wild population and > 50% of the hatchery broodstock are wild fish)	Ph > 0.75		x			
	0.75 > Ph > 0.30			x		
	0.10 > Ph < 0.30				x	
	0.05 > Ph > 0.10					x
	Ph < 0.05					x
Low (Broodstock source is from same stratum or from same wild population but < 50% wild fish used as hatchery broodstock)	Ph > 0.75	x				
	0.75 > Ph > 0.30		x			
	0.10 > Ph < 0.30			x		
	0.05 > Ph > 0.10				x	
	Ph < 0.05					x
Very Low (Broodstock source is from different stratum or ESU)	Ph > 0.75	x				
	0.75 > Ph > 0.30	x				
	0.10 > Ph < 0.30		x			
	0.05 > Ph > 0.10			x		
	Ph < 0.05				x	

Anthropogenic Mortality

Anthropogenic mortality (e.g., from harvest or habitat alterations) is unlikely to be selectively neutral. The susceptibility to mortality will differ depending on size, age, run timing, disease resistance or other traits. The TRT developed general guidelines for relating anthropogenic mortality to extinction risk category (Table 11). Different types of mortality will certainly have different selective effects and therefore different impacts on extinction risk and these guidelines are only a starting point for the consideration of this risk.

Table 11: Relationship between anthropogenic mortality and persistence category.

Anthropogenic Mortality Rate (%)[1]	Persistence Category				
	0	1	2	3	4
> 95%	x				
80%-95%		x			
45%-80%			x		
20%-45%				x	
< 20%					x

[1] Includes anthropogenic factors that could potentially result in non-random mortality (harvest, hydro operations, etc.). Adjust +/- depending on the presumed strength of selection (e.g., seasonal temporal selection, gill net size selection).

Habitat Diversity

Habitat characteristics have clear selective effects on populations and changes in habitat characteristics are expected to eventually lead to genetic changes through selection for locally adapted traits (although habitat changes can occur at a much faster rate than genetic changes, as a result the fitness of a population is rarely optimized as it adjusts to a constantly moving target). Therefore, change in habitat diversity is a reasonable surrogate for evaluating potential changes in population diversity. In assessing risk associated with altered habitat diversity, we take the historical diversity as a reference point here and throughout this evaluation. The topic is discussed elsewhere in this report. In the viability report, we developed two simple habitat diversity metrics. One metric is based on the distribution of accessible habitats at different elevations and the other is based on the distribution of accessible habitats of different stream size. The viability report describes how these metrics are related to the persistence categories and provides a table of habitat diversity scores in the viability report Appendix I.

Integrating the Diversity Factors

Few of the population diversity assessments contained sufficient information on each of the factors to utilize a single mathematical algorithm to integrate the scores. For each population, those factors that were scored were averaged. Consideration was given to the quality of data used to determine each factor. Information on data quality is given in the diversity summary for each population.

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